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Diversity of soil bacteria and fungi communities in artificial forests of the sandy-hilly region of Northwest China

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Abstract: Soil erosion is a serious issue in the sandy-hilly region of Shanxi Province, Northwest China. There has been gradual improvement due to vegetation restoration, but soil microbial community characteristics in different vegetation plantation types have not been widely investigated. To address this, we analyzed soil bacterial and fungal community structures, diversity, and microbial and soil environmental factors in *Caragana korshinskii* Kom., *Populus tomentosa* Carr., *Populus simonii* Carr., *Salix matsudana* Koidz, and *Pinus tabulaeformis* Carr. forests. There were no significant differences in the dominant bacterial community compositions among the five forest types. The alpha diversity of the bacteria and fungi communities showed that ACE (abundance-based coverage estimator), Chao1, and Shannon indices in *C. korshinskii* forest were significantly higher than those in the other four forest types ($P < 0.05$). Soil organic matter, total nitrogen, and urease had a greater impact on bacterial community composition, while total nitrogen, β -glucosidase, and urease had a greater impact on fungal community composition. The relative abundance of beneficial and pathogenic microorganisms was similar across all forest types. Based on microbial community composition, diversity, and soil fertility, we ranked the plantations from most to least suitable as follows: *C. korshinskii*, *S. matsudana*, *P. tabulaeformis*, *P. tomentosa*, and *P. simonii*.

Keywords: microbial community composition; artificial forest; bacteria; fungi; diversity; sandy-hilly region

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1 Introduction

Soil microorganisms play critical roles in soil nutrient cycle, structural formation, and plant interaction. These roles are important for reestablishing soil microbial function and biodiversity during ecosystem restoration (Fu et al., 2008; Cui, 2021). However, some studies have found that anthropogenic activities (e.g., afforestation) and climate change can directly or indirectly affect soil physical-chemical properties (Yang et al., 2017), and thus, affect the structure and function of soil microbial communities (Dong and Zheng, 2009; Ge et al., 2013; Sun et al., 2013; Huang et al., 2019; Zhao et al., 2020). This then affects plant productivity, as it can lead to regulatory changes

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in the availability of plant nutrients (Wu et al., 2008; Zhao et al., 2018). In arid and semi-arid areas, soil microbes play an important role in ecosystem protection and in maintaining stable productivity of plant community. In recent decades, the area of degraded land in China had a tendency to increase in relation to global climate change and intensified anthropogenic activities. Artificial vegetation has consequently become the most rapid and effective means by which to improve the ecological environment (He et al., 2005; Zhao et al., 2018). China is now reported to have planted approximately one-third of the world's total area of artificial forests (Zhang and Gao, 2000). In recent years, the effects of artificial afforestation on soil physical-chemical properties and microbial communities have received increasing attention and become a research hotspot in ecological studies.

Previous studies have examined the effects of artificial forest plantation on the structure and diversity of soil microbial communities and physical-chemical properties. For instance, Zhao et al. (2020) studied the effects of artificial *Pinus massoniana* Lamb. forests of different ages on soil microbial community structures and metabolic function diversity, and they found that forest age had a significant effect on soil microbial community structure. Yu et al. (2015) investigated the effects of artificial sea buckthorn forests of different ages in a hilly loess region, on soil microbial community structure and soil nutrient characteristics, and they found that the total phospholipid fatty acid content and total bacterial content reached their maximum when the forests were of a mature age, while the total fungi reached their maximum when the forests were of a middle age, and then decreased slightly when they were of a mature age. Wu et al. (2015) found that soil nutrient content is closely related to the functional diversity of soil microorganisms, and the decline in soil nutrient content will inevitably reduce microbial diversity. Collectively, these studies have showed that artificial forest plantation has significant effects on soil microbial community structures and diversity. However, these studies mainly focused on the impact of planting single plant species on soil microorganism communities. The impacts of different plant species plantations on microorganisms are relatively rare, and only a few studies show direct comparisons and analyses of the diversity of soil bacteria and fungi communities in different artificial forests.

The sandy-hilly region of Shanxi Province, Northwest China is a typical agriculture-pasture interlaced zone, in which soil erosion, land degradation, and blown-sand activities are severe (Wang et al., 2018). To achieve wind prevention, people planted sand fixation artificial forests in this region since the 1980s. The planted shrub species are mainly the drought-tolerant and barrenness-tolerant *Caragana korshinskii* Kom. (Liang et al., 2019), and the planted arbor species mainly include *P. tomentosa*, *P. simonii*, *S. matsudana*, and *P. tabuliformis*. A succession of ecological restoration and construction projects have clearly improved vegetation cover and alleviated soil erosion and water loss in the sandy-hilly region. Previous studies on the artificial forests in this region have mainly focused on their effects on soil moisture (Zhao et al., 2004; Guo and Shao, 2010; Xu et al., 2021), soil nutrients (Chang and Yue, 2008; Zhang et al., 2011; Yu et al., 2021), and understory herbaceous plants (Zhao et al., 2011; Shu et al., 2021). Wang and Li (1989) and Liang et al. (2014) investigated the characteristics of soil moisture content in artificial *C. korshinskii* forests of different ages in the sandy-hilly region. Their results showed that soil moisture content tends to decrease with the increase in age of the artificial *C. korshinskii* forests. Liu et al. (2022) researched the vegetation communities and soil properties of 50-year-old artificial *C. korshinskii* forests and found that with the increase of age, soil organic carbon, pH value, and rapidly available soil nitrogen and potassium tended to increase, while soil moisture content, salinity, and rapidly available soil phosphorus tended to decrease. In addition, the improvement in soil environment brings about a significant increase in the variety and quantity of herbaceous plants, as well as changes in the dominant species. The understory herbaceous plant species were found to be most abundant in the 30-year-old artificial *C. korshinskii* forests (Cui et al., 2018). However, relatively few studies were focused on characterizing the soil bacterial and fungal communities in different artificial forests in the sandy-hilly region. In this study, we have

comparatively analyzed the main artificial *C. korshinskii*, *P. tomentosa*, *P. simonii*, *S. matsudana*, and *P. tabuliformis* plantations in the sandy-hilly region based on soil bacterial and fungal community composition and diversity, and the relationship between soil microorganisms and soil environmental factors. The objective of this study was to provide a scientific basis for the maintenance and cultivation of soil fertility, the conservation of soil microbial diversity, and comprehensive ecological governance for the agriculture-pasture interlaced zone of Shanxi Province, Northwest China.

2 Materials and methods

2.1 Study area

The study area was located in the Shizuitou Village, Xinzhou City, Shanxi Province, China (38°44′–39°17′N, 111°28′–113°00′E; 1200–1400 m a.s.l.). The region is dominated by a temperate continental monsoon climate, with frequent sandstorms in spring and most rainfall occurring from June to September. The average annual wind speed is 2.8 m/s, annual precipitation is approximately 400 mm, annual evaporation is 1913 mm, and daily mean temperature is 4.1°C–5.5°C. The main soil type is loess-like light chestnut brown soil, with a loose texture, high porosity, and low fertility. The main artificial arbor species planted in the sandy-hilly region include *P. simonii*, *P. tomentosa*, *S. matsudana*, and *P. tabuliformis*, while the main shrub species is *C. korshinskii* and the understory herbaceous plants include *Bothriochloa ischaemum* (L.) Keng, *Artemisia* spp. and *Agriophyllum squuosun* (L.) Moq. The morphological characteristics of the arbor and shrub species are presented in Table 1.

Table 1 Morphological characteristics of dominant plant species

| Indicator | CK (<i>Artemisia dalailamae</i>) | <i>Caragana</i> <i>korshinskii</i> | <i>Populus</i> <i>tomentosa</i> | <i>Populus</i> <i>simonii</i> | <i>Salix</i> <i>matsudana</i> | <i>Pinus</i> <i>tabuliformis</i> |
|--------------------|---------------------------------------|---------------------------------------|------------------------------------|----------------------------------|----------------------------------|-------------------------------------|
| Plant height (m) | 0.42±0.02 ^d | 2.21±0.03 ^d | 5.67±0.50 ^c | 7.12±0.25 ^b | 5.50±0.60 ^c | 12.33±0.33 ^a |
| Crown breadth (m) | 0.21±0.02 ^c | 3.10±0.33 ^b | 2.43±0.04 ^b | 3.18±0.54 ^b | 2.33±0.10 ^b | 5.17±0.55 ^a |
| Stem diameter (cm) | 0.40±0.01 ^c | 2.86±0.07 ^b | 13.78±0.40 ^a | 16.89±1.93 ^a | 16.00±1.07 ^a | 16.33±0.88 ^a |

Note: Different lowercase letters within the same row indicate significant differences among different artificial forests at $P<0.05$ level. Mean±SD.

2.2 Collecting and pretreating soil samples

Soil samples were taken from two depths (0–10 and 10–20 cm) under the canopy at five artificial forests (*C. korshinskii*, *P. tomentosa*, *P. simonii*, *S. matsudana*, and *P. tabuliformis*) from July to October in 2019. A hand auger boring was used for sampling. The sample plots were located on the flat land between hills, and they had similar site conditions (i.e., soil matrix, vegetation, and climate). Natural recovery land with *Artemisia dalailamae* Krasch. as the dominant species was selected as a control (CK). We used a nested experimental design to randomly select three sampling sites with a similar slope degree (4°–8°) and aspect (south) of each artificial forest. The slope positions of the sampling sites were located at the top-slope, mid-slope, and down-slope of each artificial forest, which were separated by at least 200 m. Then, three 20 m×20 m quadrats, separated by at least 25 m, were set at each sampling site. At each quadrat, a 3-m-wide and 20-m-long transect was set up, and five soil samples under and between the artificial forest were collected along the transect, and then pooled to form two composite samples for each quadrat. For each artificial forest, 18 soil samples were collected, and a total of 108 soil samples were obtained. Each sample was divided into two sub-samples: one was stored at –20°C for soil DNA extraction and enzyme activity analysis, and the other was air-dried for soil physical-chemical analysis (Zhang et al., 2018).

2.3 Determining soil physical-chemical properties and enzyme activity

The determination methods used for the physical, chemical, and biological properties of the soil are described in Table 2.

Table 2 Determination methods used for various soil indices

| Type | Indicator | Determination method |
|----------------------------|----------------------|--|
| Soil physical property | Soil water | STEPS soil five-parameter analyzer (COMBI 5000, Berlin, Germany) |
| | Organic matter | Potassium dichromate oxidation-oil bath heating method (Xi et al., 2015) |
| Soil chemical properties | Total nitrogen | Semi-micro Kjeldahl method |
| | Total phosphorus | Sodium hydroxide alkali melting-molybdenum antimony anti-colorimetric method |
| | Glucosidase | Colorimetric method of nitrophenol (Xu et al., 2018) |
| Soil biological properties | Alkaline phosphatase | Colorimetric method of phenyl disodium phosphate (Liu et al., 2019) |
| | Urease | Sodium phenol-sodium hypochlorite colorimetric method |
| Soil microorganism | | Illumina MiSeq high-throughput sequencing was conducted by Beijing Baimaike Biological Co., Ltd., Beijing, China |

2.4 Soil sample DNA extraction and high-throughput sequencing

Three duplicate soil samples collected at depths of 0–10 and 10–20 cm from different artificial forests were mixed. Then, we took 0.5 g from the mixed samples for DNA (deoxyribonucleic acid) extraction using a Power Soil DNA Isolation Kit, according to the manufacturer's instructions. For the extracted genomic DNA, the 16S rDNA V3-V4 bacterial regions were amplified using the forward primer 5'-ACTCCTACGGGAGGCAGCA-3' and reverse primer 5'-GGACTACHVGGG-TWTCTAAT-3', and the ITS-ITS1 fungal regions were amplified using the forward primer 5'-CTTGGTCATTTAGAGGAAGTAA-3' and reverse primer 5'-GCTGCGTTCTTCATCGATGC-3'. PCR amplification based on primer sequences was in accordance with the following reaction conditions: pre-denaturation at 95°C for 5 min, denaturation at 95°C for 1 min, annealing at 50°C for 1 min, extension at 72°C for 1 min for 15 cycles, then heat preservation at 72°C for 7 min, and storage at 4°C. The amplification results were subjected to 2% agarose gel electrophoresis. Finally, the amplification products were subjected to Illumina MiSeq high-throughput sequencing and analysis. The sequencing and bioinformatic services for this study were provided by Beijing Biomarker Technologies Co., Ltd., Beijing, China.

2.5 Data processing and analysis

Operational taxonomic unit (OTU) analysis was conducted for the microbial communities. First, question sequences were identified using the QIIME2 (quantitative insights into microbial ecology) software by performing the following steps: (1) eliminating sequences <50 bp in length and basic groups with a sequence tail quality <20; (2) filtering the low-complexity sequences to remove sequences in non-amplified regions from the pre-processed sequences; and (3) identifying and removing the chimeras in the sequences using UCHIME v.8.1. The eligible sequences were then subjected to OTU clustering at the 97% similarity level using USEARCH v.10.0, and bacterial sequences and fungal sequences were comparatively analyzed using the Silva (<http://www.arb-silva.de/>) and Unite (Release v.8.0, <https://unite.ut.ee/>) databases, respectively. Finally, the 97% similarity level was used as a threshold to classify the OTUs.

The microbial community diversity was analyzed using the bacterial and fungal alpha diversity (including the community richness indices ACE and Chao1, and Shannon diversity index) values for the soil samples using the QIIME2.

2.6 Statistical analysis

One-way analysis of variance (ANOVA) was conducted using SPSS v.21.0 to determine the differences in the soil physical-chemical properties and soil enzyme activity at the same soil depth between different sample plots, and statistical significance was indicated at $P < 0.05$ level. Redundancy analysis (RDA) was conducted using Canoco v.4.0 to examine the relationships between soil physical-chemical properties, enzyme activity, and microbial diversity. Graphs of the dominant species composition and diversity indices at each taxonomic level were generated using

Origin v.9.0. Correlations of the bacterial and fungal community diversities with environmental factors were assessed using R v.4.1.0.

3 Results

3.1 Distribution of soil microbial communities

3.1.1 Dominant microbial communities at the phylum level

Among soil microorganisms in the five artificial forests, there were eight bacterial phyla with relative abundances >1%: Proteobacteria, Acidobacteria, Actinobacteria, Chloroflexi, Gemmatimonadetes, Bacteroidetes, Verrucomicrobia, and Rokubacteria. At the phylum level, there were no significant differences in the dominant bacterial community compositions among the five artificial forests, while the microorganisms of four phyla (Proteobacteria, Acidobacteria, Actinobacteria, and Chloroflexi) constituted the dominant bacterial communities, with collective relative abundances of approximately 79.9%–83.4%. The relative abundance of Proteobacteria was the highest (28.2%–36.9%), followed by Acidobacteria (17.8%–22.5%), Actinobacteria (15.0%–21.0%), and Chloroflexi (8.2%–13.9%; Fig. 1). Relative abundances of the bacterial communities were significantly different among the five artificial forests. The descending order for Proteobacteria in the five artificial forests was as follows: *P. tomentosa*, *C. korshinskii*, *S. matsudana*, *P. tabuliformis*, and *P. simonii*; and the values for *P. tomentosa* and *C. korshinskii* were significantly higher than those for *S. matsudana*, *P. tabuliformis*, and *P. simonii*. The relative abundance of Acidobacteria in descending order was as follows: *C. korshinskii*, *P. simonii*, *S. matsudana*, *P. tomentosa*, and *P. tabuliformis*, and the values for *C. korshinskii* and *P. simonii* were not significantly different, but were significantly higher than the value for *P. tabuliformis*. The descending order for Actinobacteria was as follows: *S. matsudana*, *P. simonii*, *P. tabuliformis*, *C. korshinskii*, and *P. tomentosa*; and values for *P. simonii*, *S. matsudana*, and *P. tabuliformis* were significantly higher than that for *P. tomentosa*. The descending order for Chloroflexi was as follows: *P. tabuliformis*, *P. simonii*, *S. matsudana*, *P. tomentosa*, and *C. korshinskii*; and the values for *P. simonii*, *S. matsudana*, and *P. tabuliformis* were significantly higher than that of *C. korshinskii* (Fig. 1a).

In the five artificial forests, the fungal phyla Ascomycota, Basidiomycota, Mortierellomycota, Glomeromycota, Chytridiomycota, Zoopagomycota, Olpidiomyota, and Kickxellomycota had relative abundance values >1%. The Ascomycota, Basidiomycota, and Mortierellomycota phyla constituted the dominant fungal communities, with collective relative abundances of approximately 66.0%–99.1%. The highest value was for Ascomycota (23.8%–75.7%), followed by Basidiomycota (5.9%–70.5%), and Mortierellomycota (0.4%–14.5%). The species composition and relative abundances of the fungal communities were significantly different among the five artificial forests. In the artificial forest of *P. tabuliformis*, the relative abundance of Basidiomycota was the highest, followed by Ascomycota. In *C. korshinskii*, *P. tomentosa*, *P. simonii*, and *S. matsudana* forests, the relative abundance of Ascomycota was the highest. In *C. korshinskii*, the relative abundance of Mortierellomycota was also quite high. The relative abundance of Ascomycota in the five artificial forests in descending order was as follows: *P. tomentosa*, *S. matsudana*, *P. simonii*, *C. korshinskii*, and *P. tabuliformis*. Its relative abundance was significantly higher in *P. tomentosa* forest compared with those of *C. korshinskii* and *P. tabuliformis*. The relative abundance of Basidiomycota in descending order was as follows: *P. tabuliformis*, *P. simonii*, *S. matsudana*, *C. korshinskii*, and *P. tomentosa*. Its relative abundance was significantly higher in the artificial forest of *P. tabuliformis* than in the other four artificial forests. The relative abundance of Mortierellomycota in descending order was as follows: *C. korshinskii*, *S. matsudana*, *P. tabuliformis*, *P. tomentosa*, and *P. simonii*. The value for *C. korshinskii* was significantly higher than that of the other four forests (Fig. 1b).

3.1.2 Dominant microbial communities at the class level

The dominant bacterial classes of five artificial forests, including Alphaproteobacteria, Gammaproteobacteria, subgroup_6, and Acidimicrobiia, were not significantly different, while the relative abundances of dominant microbial communities were significantly different ($P < 0.05$;

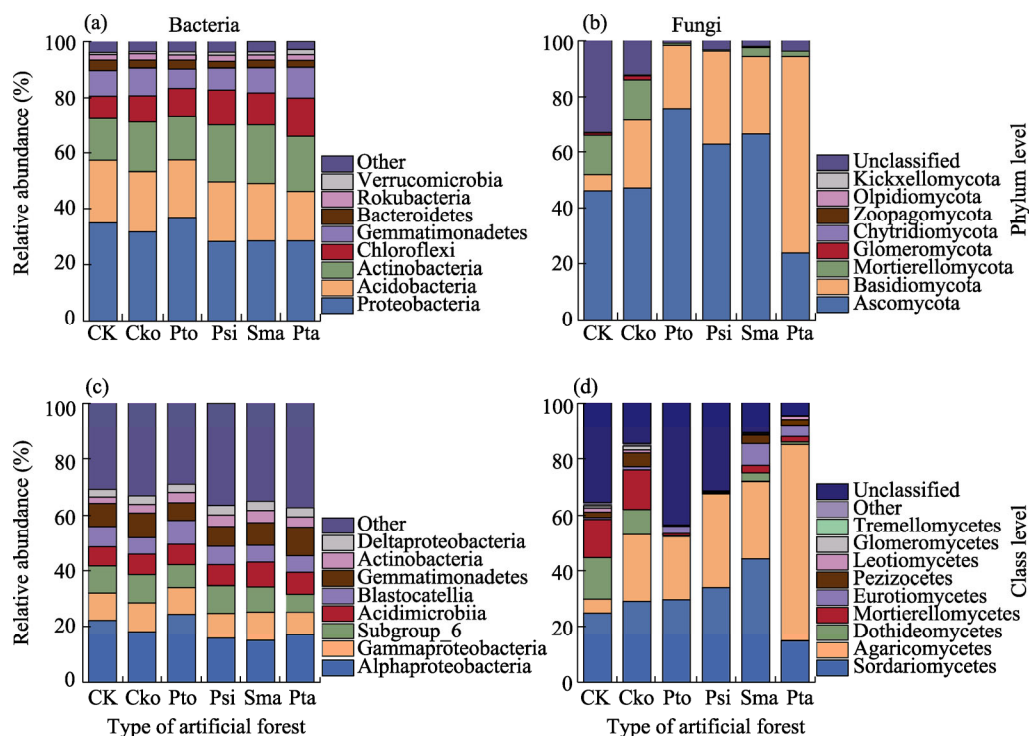


Fig. 1 Relative abundances of dominant bacteria (a and c) and fungi (b and d) at the phylum and class levels. CK, control; Cko, *Caragana korshinskii*; Pto, *Populus tomentosa*; Psi, *Populus simonii*; Sma, *Salix matsudana*; Pta, *Pinus tabulaeformis*. The abbreviations are the same as in the following figures.

Fig. 1c). The relative abundance of Alphaproteobacteria in descending order was as follows: *P. tomentosa*, *C. korshinskii*, *P. tabuliformis*, *P. simonii*, and *S. matsudana*, and the value for *P. tomentosa* was significantly higher than those of *P. tabuliformis* and *S. matsudana*. The relative abundance of Gammaproteobacteria in descending order was as follows: *C. korshinskii*, *S. matsudana*, *P. tomentosa*, *P. simonii*, and *P. tabuliformis*, and the values for *C. korshinskii* and *S. matsudana* were significantly higher than that of *P. tabuliformis*. The relative abundance of subgroup_6 in descending order is as follows: *C. korshinskii*, *P. simonii*, *S. matsudana*, *P. tomentosa*, and *P. tabuliformis*, and the value for *C. korshinskii* was significantly higher than those of other four forests. The relative abundance of Acidimicrobiia in descending order is as follows: *S. matsudana*, *P. tabuliformis*, *P. simonii*, *P. tomentosa*, and *C. korshinskii*, and the value for *S. matsudana* was significantly higher than those of other four forests.

At the class level, the dominant fungal classes of five artificial forests showed significant differences in the soils ($P < 0.05$). In *C. korshinskii*, the dominant fungal communities were Sordariomycetes, Agaricomycetes, and Mortierellomycetes, whereas in *P. tomentosa* and *P. simonii*, Sordariomycetes and Agaricomycetes were the dominant communities. However, in *S. matsudana*, the dominant fungal communities were Sordariomycetes, Agaricomycetes, and Eurotiomycetes, and in *P. tabuliformis*, Sordariomycetes were dominant (Fig. 1d). The relative abundance of Sordariomycetes in the five artificial forests was arranged in the following descending order: *S. matsudana*, *P. simonii*, *P. tomentosa*, *C. korshinskii*, and *P. tabuliformis*, while for Agaricomycetes the descending order was as follows: *P. tabuliformis*, *P. simonii*, *S. matsudana*, *C. korshinskii*, and *P. tomentosa*. The relative abundance of Dothideomycetes in descending order was as follows: *C. korshinskii*, *S. matsudana*, *P. tabuliformis*, *P. tomentosa*, and *P. simonii*; while that of Mortierellomycetes was *C. korshinskii*, *S. matsudana*, *P. tabuliformis*, *P. tomentosa*, and *P. simonii*.

3.1.3 Dominant microbial communities at the family level

At the family level, the compositions of Sphingomonadaceae, uncultured_c_subgroup_6,

Gemmatimonadaceae, and Clostridiaceae, which were the dominant bacterial communities of the five artificial forests, did not show significant differences in the soils. However, the relative abundance of the dominant bacterial families was significantly different among the five artificial forests ($P<0.05$; Table 3). The relative abundance of Sphingomonadaceae in descending order was as follows: *P. tomentosa*, *C. korshinskii*, *P. tabuliformis*, *S. matsudana*, and *P. simonii*. The relative abundance of uncultured_c_subgroup_6 in descending order was as follows: *C. korshinskii*, *P. simonii*, *S. matsudana*, *P. tomentosa*, and *P. tabuliformis*, and the value for *C. korshinskii* was significantly higher than those of other forests. The relative abundance of Gemmatimonadaceae in descending order was *P. tabuliformis*, *C. korshinskii*, *S. matsudana*, *P. simonii*, and *P. tomentosa*, and the value for *P. tabuliformis* was significantly higher than those in the other four forests. The relative abundance of Pyrinomonadaceae in descending order was as follows: *P. tomentosa*, *P. simonii*, *P. tabuliformis*, *C. korshinskii*, and *S. matsudana*, and the value for *P. tomentosa* forest was significantly higher than those of the other four forests.

The dominant fungal family of the five artificial forests was significantly different in the soils ($P<0.05$; Table 3). In *C. korshinskii*, the dominant fungal families included Inocybaceae, Mortierellaceae, and Chaetomiaceae; in *P. tomentosa*, they were Inocybaceae and Cortinariaceae; in *P. simonii*, they were Inocybaceae, Sordariaceae, and Thelephoraceae; in *S. matsudana*, they were Inocybaceae, Cortinariaceae, and Eurotiaceae; and in *P. tabuliformis*, they were Inocybaceae and Thelephoraceae. The relative abundance of Inocybaceae in descending order was as follows: *P. tabuliformis*, *P. simonii*, *C. korshinskii*, *S. matsudana*, and *P. tomentosa*, and the value for *P. tabuliformis* was significantly higher compared with those of other four forests. The relative abundance of Cortinariaceae in descending order was as follows: *S. matsudana*, *P. tomentosa*, *P. simonii*, *C. korshinskii*, and *P. tabuliformis*, and the value for *C. korshinskii* was significantly higher compared with those of other four forests. The relative abundance of Mortierellaceae in descending order was as follows: *C. korshinskii*, *S. matsudana*, *P. tabuliformis*,

Table 3 Dominant families and relative abundances of soil bacterial and fungal communities in different artificial forests

| Community | OTU | Classification | Relative abundances (%) | | | | | |
|-----------|-----|-------------------------|-------------------------|-----------------------------|--------------------------|------------------------|------------------------|----------------------------|
| | | | CK | <i>Caragana korshinskii</i> | <i>Populus tomentosa</i> | <i>Populus simonii</i> | <i>Salix matsudana</i> | <i>Pinus tabulaeformis</i> |
| Bacteria | 1 | Sphingomonadaceae | 14.3±2.5 ^a | 9.3±1.2 ^{ab} | 11.9±2.4 ^{ab} | 5.7±1.4 ^b | 6.1±1.1 ^b | 7.0±1.6 ^b |
| | 2 | Uncultured_c_subgroup_6 | 9.5±0.4 ^{ab} | 10.1±0.3 ^a | 8.1±0.4 ^c | 10.0±0.2 ^{ab} | 9.1±0.2 ^b | 6.4±0.1 ^d |
| | 3 | Gemmatimonadaceae | 8.3±0.5 ^{bc} | 8.9±0.4 ^{ab} | 6.4±0.5 ^c | 7.1±0.4 ^{bc} | 7.9±0.8 ^{bc} | 10.4±1.4 ^a |
| | 4 | Pyrinomonadaceae | 4.8±0.3 ^{ab} | 4.6±0.3 ^{ab} | 6.1±0.9 ^a | 4.8±0.6 ^{ab} | 4.3±0.5 ^{ab} | 4.7±0.5 ^{ab} |
| | 5 | Nitrosomonadaceae | 2.6±0.4 ^{ab} | 3.9±0.2 ^a | 2.4±0.5 ^b | 3.4±0.5 ^{ab} | 3.3±0.5 ^{ab} | 3.4±0.5 ^{ab} |
| | 6 | Uncultured_o_IMCC26256 | 2.3±0.2 ^{cd} | 2.6±0.0 ^{bc} | 1.8±0.1 ^d | 2.2±0.1 ^{cd} | 3.3±0.4 ^a | 2.1±0.0 ^{cd} |
| | 7 | Uncultured_c_KD4-96 | 1.6±0.1 ^c | 2.3±0.1 ^{bc} | 2.9±0.5 ^{ab} | 4.1±0.5 ^a | 2.6±0.2 ^{bc} | 4.1±0.0 ^a |
| Fungi | 1 | Inocybaceae | 3.8±2.1 ^{bc} | 17.1±9.4 ^b | 11.6±3.5 ^{bc} | 19.4±1.8 ^b | 12.3±3.0 ^{bc} | 39.8±4.4 ^a |
| | 2 | Cortinariaceae | 0.0±0.0 ^b | 0.1±0.0 ^b | 7.8±4.8 ^{ab} | 5.3±2.2 ^{ab} | 11.9±5.0 ^a | 0.0±0.0 ^b |
| | 3 | Mortierellaceae | 14.9±6.6 ^a | 14.5±3.1 ^a | 0.7±0.2 ^b | 0.4±0.1 ^b | 2.3±0.6 ^b | 1.7±0.1 ^b |
| | 4 | Chaetomiaceae | 13.3±2.3 ^a | 12.1±3.0 ^a | 0.1±0.0 ^b | 0.1±0.0 ^b | 1.0±0.3 ^b | 0.5±0.1 ^b |
| | 5 | Thelephoraceae | 0.2±0.1 ^c | 2.4±1.1 ^c | 3.0±0.8 ^c | 6.9±1.3 ^b | 3.2±0.6 ^c | 18.1±2.2 ^a |
| | 6 | Sordariaceae | 0.0±0.0 ^b | 0.1±0.0 ^b | 2.3±1.5 ^b | 13.5±6.3 ^a | 4.9±3.1 ^{ab} | 0.0±0.0 ^b |
| | 7 | Nectriaceae | 4.2±1.7 ^{ab} | 5.8±1.8 ^a | 0.2±0.1 ^c | 0.1±0.0 ^c | 1.0±0.3 ^c | 1.7±0.2 ^{bc} |

Note: OTU, operational taxonomic unit. Different lowercase letters within the same row indicate significant differences among different artificial forests at $P<0.05$ level. Mean±SD.

P. tomentosa, and *P. simonii*, and the value for *C. korshinskii* was significantly higher compared with those of other four forests. The relative abundance of Chaetomiaceae in descending order

was as follows: *C. korshinskii*, *S. matsudana*, *P. tabuliformis*, *P. tomentosa* and *P. simonii*, and the value for *C. korshinskii* was significantly higher compared with those of the other four forests.

3.1.4 Dominant microbial communities at the genus level

At the genus level, five artificial forests did not show significant differences in the dominant genera ($P>0.05$). The dominant bacterial genera were uncultured_c_subgroup_6, *Sphingomonas*, uncultured_bacterium_f_Gemmatimonadaceae, and *RB41*.

The dominant fungal genera of the five artificial forests showed significant differences in the soils ($P<0.05$; Fig. 2a). At the natural recovery plot (CK), *Mortierella* and *Chaetomium* were the dominant genera, whereas *Inocybe* and *Mortierella* were the dominant genera in *C. korshinskii*. In *P. tomentosa*, *P. simonii*, and *S. matsudana*, *Inocybe* and *Cortinarius* were the dominant genera; *Inocybe* and *Tricholoma* were the dominant genera in *P. tabuliformis* (Fig. 2b). In *P. tabuliformis*, the *Inocybe* was significantly higher than those of the other four forests. In *C. korshinskii*, *Mortierella* and *Cladosporium* were significantly higher than those of the other four forests.

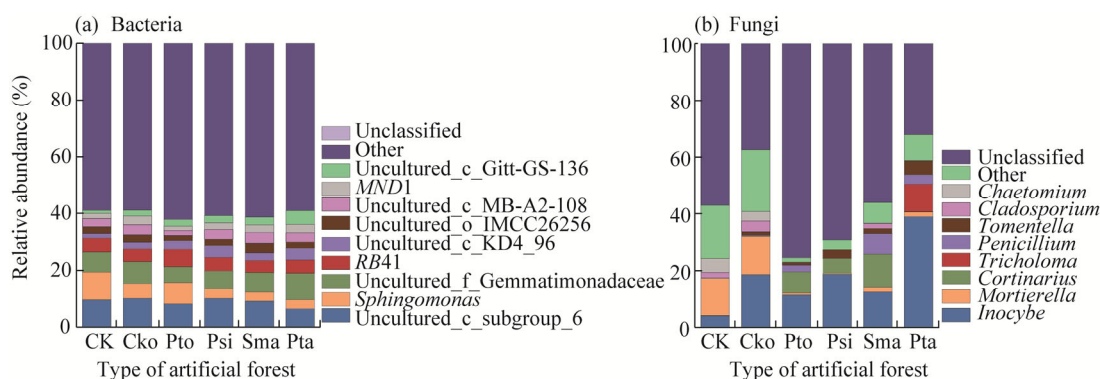


Fig. 2 Relative abundances of dominant bacteria (a) and fungi (b) at the genus level

3.2 Alpha diversity of soil microbial communities

We subjected eligible sequences to OTU clustering based on their 97% similarity levels. The alpha diversity of the soil bacterial and fungal communities in the five forests is shown in Figure 3. ACE and Chao1 indices are used to measure the species richness of a community. The higher the two indices, the higher the species richness of a community. The higher the Shannon index, the higher the community diversity. The alpha diversity of the soil microbial communities was significantly different among the five artificial forests ($P<0.05$). The richness and diversity of the soil bacterial and fungal communities in different forests are shown in Figure 4. ACE and Chao1 indices of the soil bacterial communities in the five artificial forests in descending order were as follows: *C. korshinskii*, *S. matsudana*, *P. tabuliformis*, *P. simonii*, and *P. tomentosa*. ACE and Chao1 indices of the soil bacterial communities were significantly higher in *C. korshinskii* compared with those of the other four forests ($P<0.05$), but were not significantly different between them (Fig. 3a and b). Shannon index for the soil bacterial communities in descending order was as follows: *C. korshinskii*, *S. matsudana*, *P. simonii*, *P. tabuliformis*, and *P. tomentosa*. Specifically, the Shannon index of the soil bacterial communities was significantly higher in *C. korshinskii* than those of the other four forests (Fig. 3c).

ACE index for the soil fungal communities in descending order was as follows: *C. korshinskii*, *S. matsudana*, *P. tomentosa*, *P. tabuliformis*, and *P. simonii*, and the value for *C. korshinskii* was significantly higher than those of the other four forests ($P<0.05$), which were not significantly different (Fig. 3d). Chao1 index of the soil fungal communities in descending order was as follows: *C. korshinskii*, *S. matsudana*, *P. tabuliformis*, *P. tomentosa*, and *P. simonii*, and the value for *C. korshinskii* was significantly higher than those of the other four forests (Fig. 3e). The Shannon indices for the soil fungal communities in descending order are as follows: *C. korshinskii*, *P. tabuliformis*, *S. matsudana*, *P. simonii*, and *P. tomentosa*, and the value for *C. korshinskii* was significantly higher than those of the other four forests (Fig. 3f). Overall, the

richness and diversity of the soil bacterial and fungal communities were the highest in *C. korshinskii*, followed by *S. matsudana*, and the values were relatively low in *P. tomentosa* and *P. simonii*.

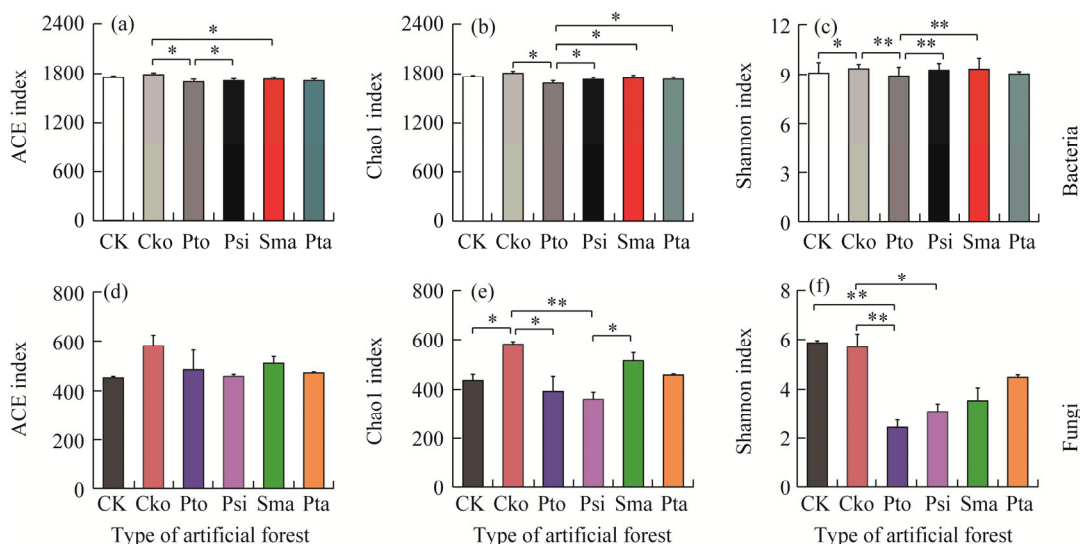


Fig. 3 Variations in ACE (abundance-based coverage estimator) (a and d), Chao1 (b and e), and Shannon (c and f) indices of the bacterial and fungal communities in different artificial forests. *, $P < 0.05$ level; **, $P < 0.01$ level.

3.3 Beta diversity of soil microbial communities

For the five artificial forest, the inter-group differences in their bacterial and fungal communities were greater than their intra-group differences ($R^2 = 0.246$ and $R^2 = 0.809$, respectively), and the differences were significant ($P < 0.05$; Fig. 4). The differences in beta diversity for the bacterial communities between *C. korshinskii* and *P. tomentosa* forests were more significant than those among *P. simonii*, *S. matsudana*, and *P. tabuliformis*, and there were only slight differences in the beta diversity of the bacterial communities among *P. simonii*, *S. matsudana*, and *P. tabuliformis* (Fig. 4a). The differences in beta diversity for the fungal communities between *C. korshinskii* and *P. tomentosa* were more significant than those between *S. matsudana* and *P. tabuliformis*, and there were only slight differences between *S. matsudana* and *P. tabuliformis* (Fig. 4b).

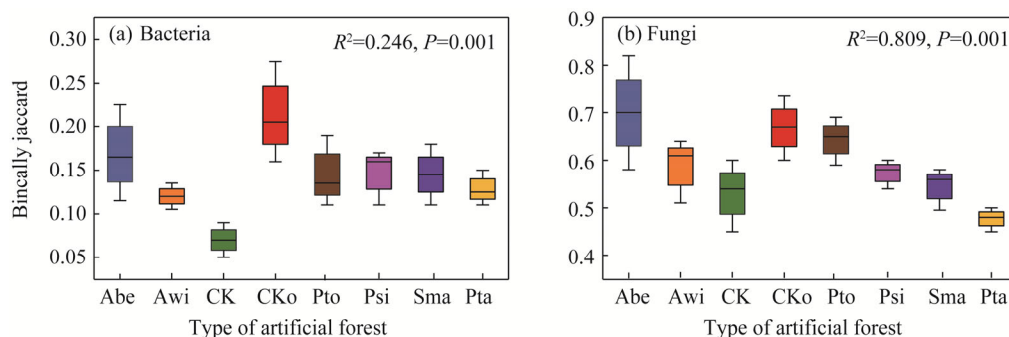


Fig. 4 Beta diversity of soil bacterial (a) and fungal (b) communities in different artificial forests. Abe (all between) represents beta distance data of samples between all groups; Awi (all within) represents beta distance data of samples within all groups. In box-plot, the five lines from bottom to top represent the minimum, lower quartile, median, upper quartile, and the maximum, respectively.

3.4 Soil physical-chemical properties

Soil physical-chemical properties, such as soil moisture, total nitrogen, and total phosphorus were

significantly affected by the five artificial forests. At the 0–10 cm depth, soil moisture content in descending order was as follows: *P. tomentosa*, *P. simonii*, CK, *P. tabuliformis*, *S. matsudana*, and *C. korshinskii*. At the 10–20 cm depth, soil moisture content in descending order was as follows: CK, *P. tomentosa*, *P. tabuliformis*, *S. matsudana*, *P. simonii*, and *C. korshinskii*. Soil moisture content was significantly lower in *C. korshinskii* compared with that in *P. tomentosa* at the 0–10 and 10–20 cm depths ($P < 0.05$; Fig. 5a). At the 0–10 cm depth, soil total nitrogen content was significantly affected by the five artificial forests. The soil total nitrogen contents in *P. tomentosa*, *P. simonii*, and *S. matsudana* were significantly higher than those in *C. korshinskii* and *P. tabuliformis*, and reached the lowest value in *C. korshinskii*. At the 10–20 cm depth, soil total nitrogen content was not significantly different among the five artificial forests (Fig. 5b). At the 0–10 and 10–20 cm depths, soil organic matter content was not significantly affected by the five artificial forests. However, soil organic matter content of the five forests was significantly lower than that of CK (Fig. 5c). At the 0–10 cm depth, soil total phosphorus content was significantly affected by the five artificial forests. Soil total phosphorus contents in *P. tomentosa* and *P. simonii* were significantly higher than those in *C. korshinskii* and *P. tabuliformis*, and the maximum and minimum values were found in *P. simonii* and *P. tabuliformis*, respectively. At the 10–20 cm depth, soil total phosphorus content was not significantly affected by the five artificial forests (Fig. 5d).

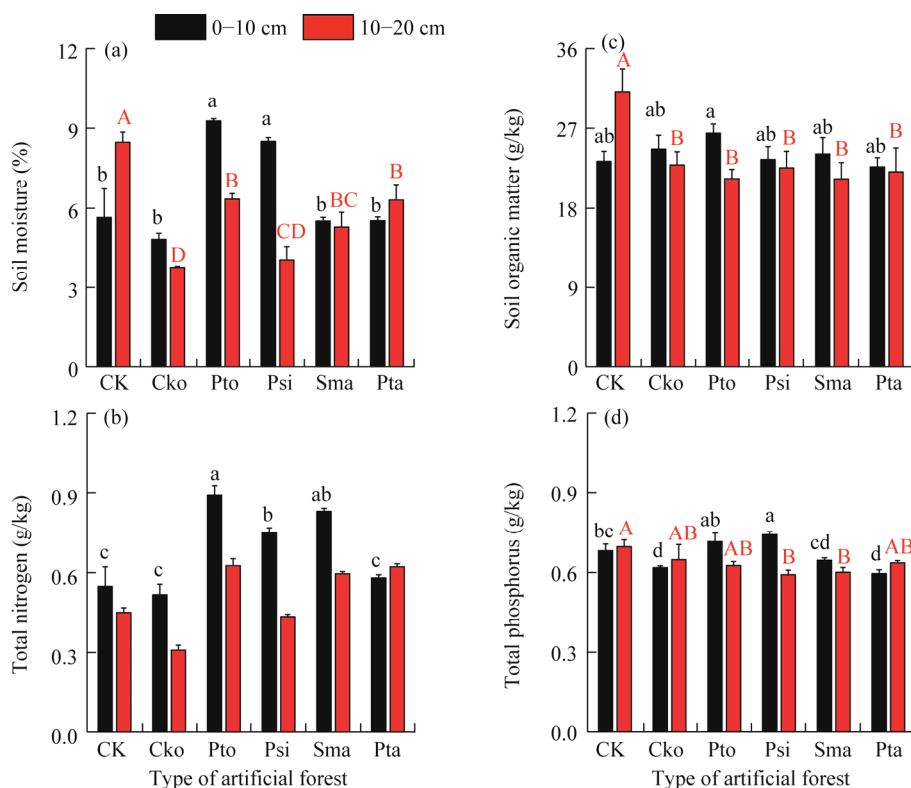


Fig. 5 Changes in soil physical-chemical properties in different artificial forests. (a), soil moisture; (b), soil organic matter; (c), total nitrogen; (d), total phosphorus. Different lowercase and uppercase letters within the same soil depth indicate significant differences among different artificial forests at $P < 0.05$ level.

3.5 Soil enzyme activity

Soil β -glucosidase and urease activities were significantly affected by the five artificial forests ($P < 0.05$). At the 0–10 cm depth, soil β -glucosidase was not significantly affected. However, they were both higher than CK. The lowest and highest β -glucosidase activities were obtained in CK and *S. matsudana*, respectively. At the 10–20 cm depth, soil β -glucosidase was significantly

affected by the five artificial forests. The values in descending order were as follows: *P. tomentosa*, *S. matsudana*, *P. tabuliformis*, *P. simonii*, and *C. korshinskii*. β -glucosidase in *P. tomentosa* and *S. matsudana* was significantly higher than that in *C. korshinskii*, *P. simonii*, and *P. tabuliformis* (Fig. 6a). Soil urease activity was significantly affected by the five artificial forests at the 0–10 and 10–20 cm soil depths. At the 0–10 cm depth, urease activity in descending order was as follows: CK, *S. matsudana*, *C. korshinskii*, *P. simonii*, *P. tabuliformis*, and *P. tomentosa*. At the 10–20 cm depth, the descending order of urease activity was as follows: CK, *C. korshinskii*, *S. matsudana*, *P. simonii*, *P. tomentosa*, and *P. tabuliformis* (Fig. 6b). Alkaline phosphatase activity was not significantly affected by the five artificial forests at the 0–10 and 10–20 cm depths. However, they were significantly lower than CK (Fig. 6c). Overall, the activity of soil β -glucosidase was higher than those of ALP and urease. Planting artificial forests can improve soil β -glucosidase.

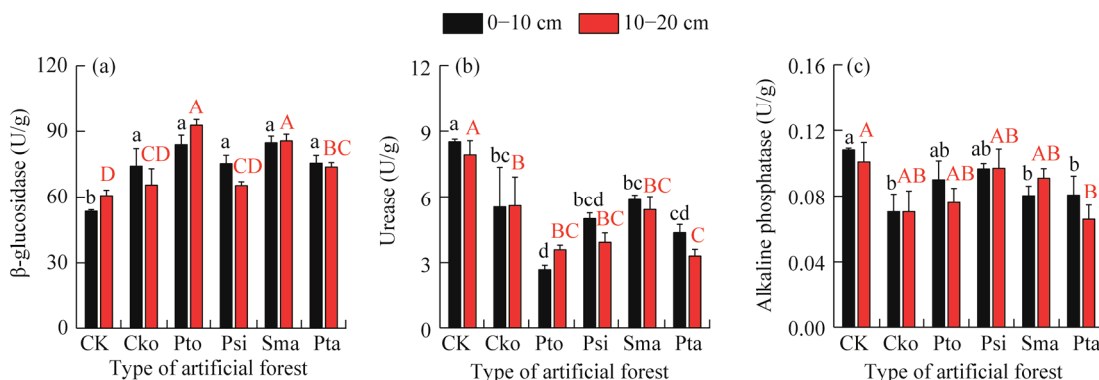


Fig. 6 Changes in soil enzyme activities in different artificial forests. (a), β -glucosidase; (b), urease; (c), alkaline phosphatase. Different lowercase and uppercase letters within the same soil depth indicate significant differences among different artificial forests at $P < 0.05$ level. Bars are standard errors.

3.6 Effects of environmental factors

The correlation matrix between bacterial community diversity index and environmental factors showed that soil bacterial diversity was correlated with soil environmental factors. For the soil bacterial communities, ACE index was very significantly and positively correlated with Chao1 and Shannon indices, and significantly and negatively correlated with total nitrogen content. Chao1 index was significantly and negatively correlated with soil moisture content, and very significantly and negatively correlated with total nitrogen content (Table 4). The correlation matrix between the fungal community diversity index and environmental factors showed that ACE index of the soil fungal communities was significantly and negatively correlated with total phosphorus content and alkaline phosphatase activity. Shannon index was very significantly and positively correlated with urease activity (Table 5). Overall, soil moisture content and total nitrogen content were identified as key environmental factors affecting bacterial community abundance and diversity, as well as total phosphorus content, whereas alkaline phosphatase and urease activities were identified as important environmental factors affecting fungal community abundance and diversity.

To examine the correlation between microbial community composition and soil environmental factors, we conducted RDA analysis using genus-level microbial communities as response variables and soil physical, chemical, and biological properties as environmental explanatory variables. The results of RDA analysis between bacterial community structure and soil environmental factors showed that the cumulative explanatory power of the first and second axes in the bacterial communities were 67.6% and 88.8%, respectively. The main environmental factors affecting the bacterial community structures included total phosphorus content, organic matter content, and urease activity. Dominant bacterial genera including uncultured_c_subgroup_6,

Table 4 Correlations between bacterial community diversity indices and environmental factors

| Index | ACE | Chao1 | Shannon | Soil moisture | SOM | TN | TP | β -glucosidase | ALP | Urease |
|----------------------|--------|--------|---------|---------------|-------|--------|--------|----------------------|------|--------|
| ACE | 1.00 | | | | | | | | | |
| Chao1 | 0.99** | 1.00 | | | | | | | | |
| Shannon | 0.72* | 0.72* | 1.00 | | | | | | | |
| Soil moisture | -0.66 | -0.75* | -0.61 | 1.00 | | | | | | |
| SOM | 0.19 | 0.15 | -0.38 | 0.22 | 1.00 | | | | | |
| TN | -0.74* | -0.78* | -0.32 | 0.68* | -0.24 | 1.00 | | | | |
| TP | -0.49 | -0.55 | -0.49 | 0.70* | 0.39 | 0.22 | 1.00 | | | |
| β -glucosidase | -0.65 | -0.63 | -0.20 | 0.29 | -0.37 | 0.86** | -0.14 | 1.00 | | |
| ALP | -0.26 | -0.28 | -0.17 | 0.23 | 0.18 | -0.02 | 0.77** | -0.29 | 1.00 | |
| Urease | 0.65 | 0.55 | 0.41 | 0.10 | 0.47 | -0.22 | 0.07 | -0.51 | 0.05 | 1.00 |

Note: ACE, abundance-based coverage estimator; SOM, soil organic matter; TN, total nitrogen; TP, total phosphorus; ALP, alkaline phosphatase. *, $P < 0.05$ level; **, $P < 0.01$ level.

Table 5 Correlations between fungal community diversity indices and environmental factors

| Index | ACE | Chao1 | Shannon | Soil moisture | SOM | TN | TP | β -glucosidase | ALP | Urease |
|----------------------|---------|---------|---------|---------------|-------|--------|--------|----------------------|------|--------|
| ACE | 1.00 | | | | | | | | | |
| Chao1 | 0.84** | 1.00 | | | | | | | | |
| Shannon | 0.28 | 0.63 | 1.00 | | | | | | | |
| Soil moisture | -0.59 | -0.49 | -0.08 | 1.00 | | | | | | |
| SOM | -0.06 | 0.08 | 0.40 | 0.22 | 1.00 | | | | | |
| TN | -0.28 | -0.23 | -0.46 | 0.68* | -0.24 | 1.00 | | | | |
| TP | -0.72* | -0.78** | -0.26 | 0.70* | 0.39 | 0.22 | 1.00 | | | |
| β -glucosidase | 0.11 | -0.02 | -0.61 | 0.29 | -0.37 | 0.86** | -0.14 | 1.00 | | |
| ALP | -0.76** | -0.75* | -0.34 | 0.23 | 0.18 | -0.02 | 0.77** | -0.29 | 1.00 | |
| Urease | 0.09 | 0.46 | 0.83** | 0.10 | 0.47 | -0.22 | 0.07 | -0.51 | 0.05 | 1.00 |

Note: *, $P < 0.05$ level; **, $P < 0.01$ level.

Sphingomonas, and uncultured_bacterium_f_Gemmatimonadaceae in the five forests were positively correlated with soil total phosphorus content, organic matter content, and urease activity (Fig. 7a).

For the abundance of soil fungal communities, the cumulative explanatory power of the first and second axes was 53.9% and 84.5%, respectively. The main environmental factors affecting the fungal community structures included total nitrogen content, organic matter content, β -glucosidase activity, and urease activity (Fig. 7b). The dominant fungal genera including *Inocybe*, *Mortierella*, and *Cladosporium* in *C. korshinskii* were significantly correlated with organic matter content, urease activity, and β -glucosidase activity. Dominant fungal genera including *Inocybe*, *Cortinarius*, and *Penicillium* in *P. tomentosa* and *S. matsudana* were significantly correlated with total nitrogen content. Dominant fungal genera including *Inocybe*, *Cortinarius*, and *Tomentella* in *P. simonii* were correlated with β -glucosidase activity. Dominant fungal genera including *Inocybe*, *Tricholoma*, and *Tomentella* in *P. tabuliformis* were significantly correlated with β -glucosidase activity.

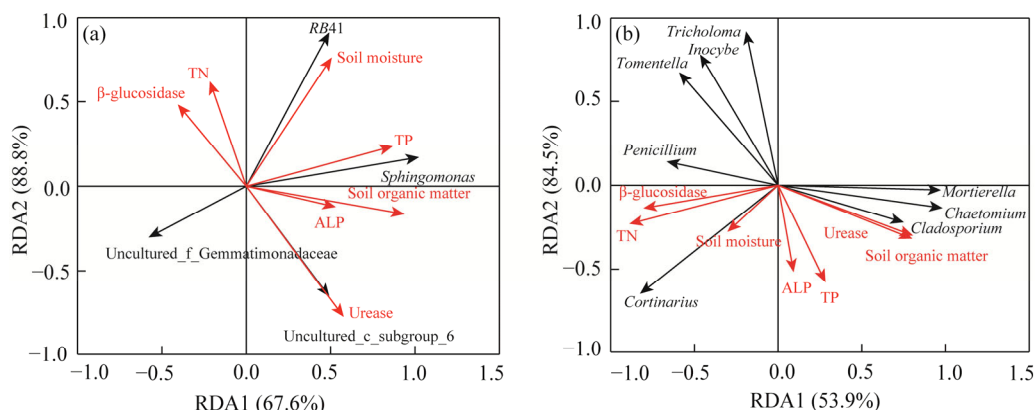


Fig. 7 RDA (redundant analysis) of dominant bacteria (a) and fungi (b) species composition and soil environmental factors. Black arrows denote dominant microbial species, and red arrows denote soil environmental factors. ALP, alkaline phosphatase. TP, total phosphorus; TN, total nitrogen.

4 Discussion

4.1 Effects of different artificial forests on soil microbial community composition

The dominant bacterial phyla in the artificial *C. korshinskii*, *P. tomentosa*, *P. simonii*, *S. matsudana*, and *P. tabuliformis* forests were found to be Proteobacteria, Acidobacteria, Actinobacteria, and Chloroflexi, and their relative abundance levels differed significantly among five forests ($P < 0.05$). These results are consistent with the findings of Wang et al. (2019), who investigated the effects of different vegetation types on soil microorganisms in the Chinese Loess Plateau. Specifically, the results of this study showed that Proteobacteria, Chloroflexi, Acidobacteria, and Actinobacteria had the highest relative abundances in *P. tomentosa*, *P. tabuliformis*, *C. korshinskii*, and *S. matsudana* forests, respectively. The dominant fungal phyla included Ascomycota, Basidiomycota, and Mortierellomycota, and these results are consistent with the conclusions of Huang et al. (2018) for soil microorganisms in arid and semi-arid regions. Basidiomycota had the highest abundance in *P. tabuliformis*, followed by Ascomycota. In the other four forests, the relative abundance of Ascomycota was the highest, whereas that of Mortierellomycota was relatively high in *C. korshinskii*. Due to the differences in ground vegetation, dry branches, fallen leaves, and root exudates varied among the five artificial forests and changed the soil physical-chemical properties. The composition and relative abundance of soil microbial communities was thus also expected to be different among the five artificial forests (Zhang et al., 2002; Wu et al., 2008).

The dominant bacterial genera in the five artificial forests were not significantly different and included *uncultured_c_subgroup_6*, *Sphingomonas*, *uncultured_f_Gemmatimonadaceae*, and *RB41*. In contrast, the dominant fungal genera differed in composition among different artificial forests, and these included *Inocybe*, *Mortierella*, *Cortinarius*, *Tricholoma*, and *Penicillium*. These results showed that different artificial forests affected fungal communities more significantly than bacterial communities, and that bacterial communities were relatively stable in the five artificial forests. These results are different from those of Deng et al. (2020) and Wang et al. (2020). Deng et al. (2020) investigated the composition and functional characteristics of soil fungal communities in different artificial forests in a windy and sandy region of northwestern Liaoning Province, and their results showed that the dominant fungal genera in the region included *Guehomyces*, *Mortierella*, and *Penicillium*. In contrast, Wang et al. (2020) studied the soil microorganisms in lilac shrubs in the Helan Mountains, and their results showed that the dominant bacterial genera included *Sphingomonas*, *RB41*, *Lysobacter*, and *H16*, and that the dominant fungal genera included *Clonostachys*, *Saccharomycopsis*, *Fusarium*, and *Mortierella*. These differences may reflect the heterogeneity in their habitat conditions (e.g., climate, soil,

vegetation, and landform). Microbial communities can thus respond differently to environmental factors in different land use and vegetation conditions, resulting in changes to both their number and composition.

Soil microorganisms can promote plant growth by regulating nutrient supply and metabolism, while some pathogenic microorganisms can cause plant decline or death (Ning et al., 2022). Among the microbial communities, certain bacterial (e.g., *Sphingomonas* and uncultured_f_Gemmatimonadaceae) and fungal genera (e.g., *Inocybe*, *Mortierella*, *Chaetomium*, and *Tomentella*) can promote plant growth. Specifically, *Cortinari* and *Tricholoma* are important ectomycorrhizal fungi, which can promote forest growth, improve the stress resistance of forests, and increase afforestation survival and forest productivity. Consequently, these are of vital importance for maintaining the stability of forest ecosystems (Li et al., 2018; Wang et al., 2021). *Inocybe*, *Mortierella*, and *Penicillium* have important roles in the cycling of carbon, nitrogen, and phosphorus in the soil (Peng et al., 2019; Zhang et al., 2019). The significant changes in the dominant bacterial and fungal species showed that the relative abundance of *Cladosporium* was the highest in *C. korshinskii* (Fig. 8). *Cladosporium* is a common genus of endophytic fungi, and most are saprophytic, but some cause secondary plant infections, which can produce leaf spot, leaf mold, fruit rot, stem rot, textile decay, and wood decay, leading to serious losses for agricultural products. A few *Cladosporium* fungi can also cause human and animal diseases (Jiao et al., 2019). Some studies have argued that the artificial sand-fixing *C. korshinskii* forests are characterized by strong adaptability, drought, and barren tolerance, and fast growth at the early and middle stages of planting, but face problems, such as growth slowdown, premature stand weakening, and pest and disease damage, approximately 30 a after planting. In the future,

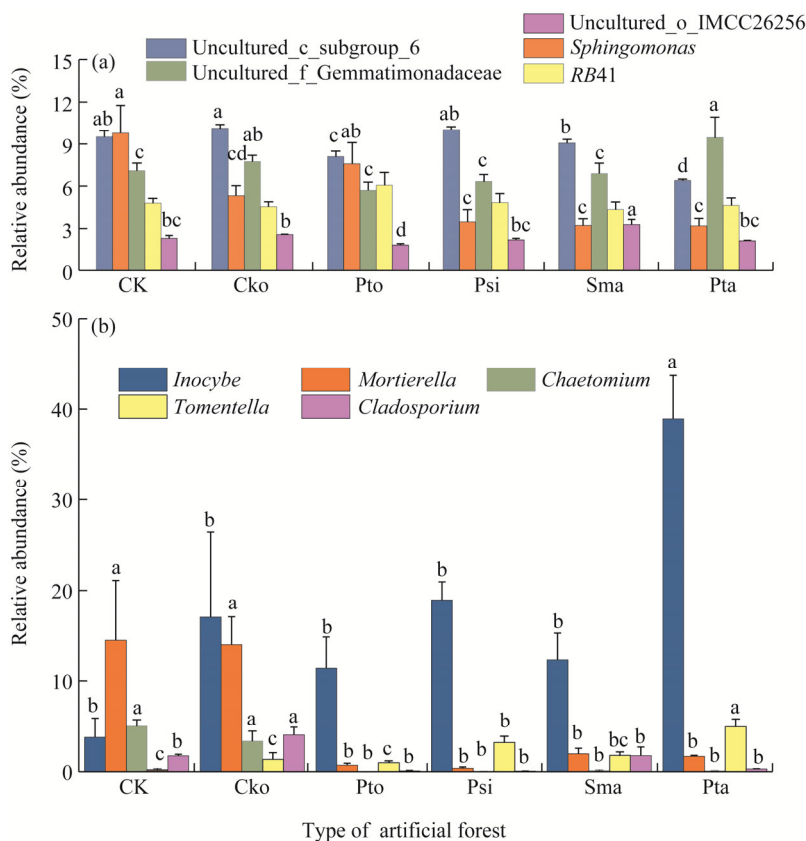


Fig. 8 Dominant species of bacterial (a) and fungal (b) communities in different artificial forests. Different lowercase letters within the same bacteria or fungi indicate significant differences among different types of artificial forests at $P < 0.05$ level. Bars are standard errors.

adverse influences of pathogenic microorganisms (e.g., *Cladosporium*) on the growth of *C. korshinskii* in northwestern Shanxi Province will need to be considered. Overall, the relative abundance of the beneficial microorganisms (e.g., *Inocybe*, *Mortierella*, *Chaetomium*, and *Tomentella*) was the highest in *P. tabuliformis*, followed by *C. korshinskii*, and the lowest in *P. tomentosa*.

4.2 Effects of different forest types on soil microbial community diversity

Previous studies have shown that land use patterns can affect soil physical-chemical properties through vegetation diversity and heterogeneity and different management measures, which subsequently affect the diversity and composition of soil microorganisms (Guo, 2017; Deng et al., 2020). This study found that the alpha diversity of soil bacterial and fungal communities was the highest in *C. korshinskii*, followed by *S. matsudana*, but was relatively low in *P. tomentosa* and *P. simonii*. This may be due to the following factors: (1) *C. korshinskii*, as a species of leguminous shrubs, has a large number of rhizobia on its roots, which can fix free nitrogen in the air and increase soil nitrogen content; and (2) *C. korshinskii* has luxuriant branches and leaves, and when they fall, they can increase soil organic matter and total nitrogen, thus improving soil fertility (Niu et al., 2003). As a result, the increased soil nutrient content can increase the abundance and diversity of soil microorganisms (Niu et al., 2003). The abundance and diversity of soil bacterial and fungal communities were relatively low in *P. tomentosa* and *P. simonii*. This is predominately because their dry branches and fallen leaves contain large quantities of slowly decomposable organic matter (e.g., lignin and cellulose) (Yang et al., 2007), which results in low soil nutrient content levels, as well as low soil microorganism abundance and diversity.

This study also found that the differences in beta diversity for the bacterial communities between *C. korshinskii* and *P. tomentosa* were more significant than those between *P. simonii*, *S. matsudana*, and *P. tabuliformis*. In addition, the differences in beta diversity for the bacterial communities were slight among *P. simonii*, *S. matsudana*, and *P. tabuliformis*. The differences in beta diversity for the fungal communities among *C. korshinskii*, *P. tomentosa* and *P. simonii* were more significant than that between *S. matsudana* and *P. tabuliformis*. In addition, the difference in beta diversity for the fungal communities was slight between *S. matsudana* and *P. tabuliformis*. These results showed that *C. korshinskii* forest exhibited significant differences but low similarities in species diversity compared with the other four forests. This may be due to the following factors: (1) with the increase in planting age, soil environment is improved, and the variety and quantity of herbaceous plants increase significantly (Liu et al., 2022); and (2) *C. korshinskii* has a well-developed root system, which positively affects the diversity of soil microbial communities. In contrast, *P. simonii*, *S. matsudana*, and *P. tabuliformis* do not have well-developed rootlets, and their artificial forests have relatively few herbaceous plants, dry branches, and fallen leaves on the earth surface, thus producing a smaller effect on the soil microorganisms.

4.3 Correlation between soil microorganisms and soil environmental factors

Usually, soil physical-chemical properties are strongly correlated with the structure and diversity of rhizospheric microbial communities. In this study, we found that the soil moisture and total nitrogen contents were key environmental factors affecting the abundance and diversity of the soil bacterial communities in Shanxi Province, and that the total phosphorus content, alkaline phosphatase activity, and urease activity were important environmental factors affecting the abundance and diversity of soil fungal communities. These results are somewhat different from the conclusions of Liu et al. (2013) and Dai et al. (2017). Dai et al. (2017) found that soil bacterial community diversity has a positive and significant correlation with soil nutrient content (e.g., organic matter content). However, Liu et al. (2013) found that soil bacterial diversity is positively correlated with soil total nitrogen, total phosphorous, and soil organic matter content, but negatively correlated with soil pH value. This may be due to the differences in the environment of different regions. This also indicates that soil microbial community diversity is not caused by a

single factor, but is related to a diverse and complex array of environmental factors.

RDA results showed that dominant bacterial species are significantly affected by soil total phosphorus content, soil organic matter content, and urease activity, and that dominant fungal species are significantly affected by soil total nitrogen content, soil organic matter content, β -glucosidase activity, and urease activity. Evidently, soil nutrient content and enzyme activity are important regulatory factors for soil microorganisms. The dominant fungal species compositions were different among five artificial forests. This was because the essential nutrients varied across different microbial species, and the environmental factors affecting soil microorganisms were found to be somewhat different among five artificial forests.

5 Conclusions

In the sandy-hilly region used in this study, planting artificial forests was found to significantly affect the composition and diversity of soil bacterial and fungal communities. Furthermore, soil nutrient content and enzyme activity levels were found to be important driving factors for the changes in soil microbial composition and diversity. Overall, artificial *C. korshinskii* forest had the highest abundance and diversity levels for soil bacterial and fungal communities, soil nutrient content, enzyme activity, and relative abundance of beneficial microorganisms. *P. tomentosa* forest was found to have high soil nutrient content and enzyme activity levels, but low abundance and diversity in terms of soil microorganisms, whereas *P. simonii* had low abundance and diversity levels for soil microorganisms, soil nutrient content, and enzyme activity. From a microbiological perspective, the most suitable plant species for this sandy-hilly region was found to be *C. korshinskii*, followed by *S. matsudana*, and *P. tabuliformis*. In contrast, neither *P. tomentosa* nor *P. simonii* were found to be beneficial for increasing soil microbial abundance and diversity in Shanxi Province. *C. korshinskii* forest also had increased soil fertility and a higher abundance of certain pathogenic microorganisms, compared with the other four artificial forests. The long-term artificial cultivation of undiversified plant species will increase pathogenic microorganisms in the soil. In the future, the management of artificial forests in Shanxi Province must focus on the effects of pathogenic microorganisms on plant growth. Moreover, mixed artificial forests with the antagonistic effects on these pathogenic microorganisms was recommended. The results of this study will provide scientific guidance to improve land management and ecological restoration in Shanxi Province, Northwest China.

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